

05-90
131

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/970,287

DATE: 10/24/2001
TIME: 16:28:57

Input Set : A:\10147611.app
Output Set: N:\CRF3\10242001\1970287.raw

3 <110> APPLICANT: GLUCKSMANN, Maria A.
4 MEYERS, Rachel
5 KAPELLER-LIBERMANN, Rosana
6 SILOS-SANTIAGO, Inmaculada
8 <120> TITLE OF INVENTION: 22437, A NOVEL HUMAN SULFATASE AND USES THEREFOR
10 <130> FILE REFERENCE: 10147-61U1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/970,287 ✓
13 <141> CURRENT FILING DATE: 2001-10-03
15 <150> PRIOR APPLICATION NUMBER: US 60/257,082
16 <151> PRIOR FILING DATE: 2000-12-21
18 <160> NUMBER OF SEQ ID NOS: 12
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3513
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
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30 cgtgcacaca aggtctggc tcgttccct ccctcggtt cagctctgg gcaatccca 180
31 catctgtttc aactctccgc cgagggcggag caggagcggag agtgtgtcgat atctgcgagt 240
32 gaagaggac gaggaaagaa aaacaaagcc acagacgca cttgagactc ccgcacccca 300
33 aaagaacac cagatcagca aaaaagaag atggggcccccc cgagctctgt gctgtgtttg 360
34 ctgtccgcaa ctgtgttctc cctgtgggt ggaagctgg cttctctgtc gcaccaccgc 420
35 ctgaaaggca ggttcagag ggaccgcagg aacatccgac ccaacatcat cttgtgtctg 480
36 acggacgacc aggtgtggc gctgggttcc atgcagggtga tgaacaagac ccggcgcac 540
37 atggagcagg gccccggcga cttcatcaac gccttcgtga ccacacccat gtgtgtcccc 600
38 tcacgtctt ccatcctc acggcaagtac gtccacaacc acaacaccta caccaacaat 660
39 gagaactgtt ctcgcgcctc ctggcaggca cagcacgaga gccgoaccc ttccgtgtac 720
40 ctcaatagca ctggctaccg gacagtttc ttctggaaagt atcttaatga atacaacggc 780
41 tcctacgtgc caccggctg gaaggagtgg gtcggactcc ttaaaaactc cogctttat 840
42 aactacacgc tttgtcgaa cgggggtgaaa gagaagcactg gtcggacta ctccaaaggat 900
43 tacctcacag acctcatcac caatgacagc gtggacttcc tccgcacgtc caagaagatg 960
44 tacccgcaca ggccagtcct catggtcatac agccatgcag ccccccacgg ccctgaggat 1020
45 tcagccccac aatattcagc cctctccca aacgcacatc agcacatcac gcccggactac 1080
46 aactacgcgc ccaacccggc caaacactgg atcatgcgtc acacggggcc catgaagccc 1140
47 atccacatgg aattcaccaa catgctccag cggaaagcgtc tgcagacccat catgtcggt 1200
48 gacgactcca tggagacgtt ttacacatg ctgggtgaga cggggcggact ggacaaacacg 1260
49 tacatcgat acaccggccga ccacggttac cacatggcc agtttggcct ggtgaaagg 1320
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53 gacacggagc ggccgggtgaa tcgggttcac ttgaaaaaaa agatgagggt ctggcgggac 1560
54 tccttcttgg tggagagagg caagctgctt cacaagagag acaatgacaa ggtggacgac 1620
55 caggaggaga actttctgcc caagtaccag cgtgtgaagg acctgtgtca gcgtgtctg 1680
56 taccagacgg cgtgtgagca gctggacag aagtggcagt gtgtggagga cggccacgggg 1740
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ENTER

ENTERED

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Input Set : A:\10147611.app
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58 aacctcggtc ccaagtacta cgggcaggc agcgaggcct gcacctgtga cagcggggac 1860
59 tacaagctca gcctggccgg acgcccggaa aaactttca agaagaagta caaggccagc 1920
60 tatgtccgca gtcgctccat ccgctcagtg gccatcgagg tgacggcag ggtgtaccac 1980
61 gttaggcctgg gtatggccgc ccagcccgaa aacctccatca agcggcactg gccagggggc 2040
62 cctgaggacc aagatgacaa ggtatggtggg gacttcagtg gcactggagg cttcccgac 2100
63 tactcagccg ccaacccat taaagtgaca catcggtct acatctaga gaacgacaca 2160
64 gtccagtgtg acctggacccgtc gtacaagtcc ctgcaggcct gaaaagacca caagctgcac 2220
65 atcgaccacg agattgaaac cctgcagaac aaaatttataaaga acctgaggaa agtccgaggt 2280
66 cacctgaaga aaaagccggcc agaagaatgt gactgtcaca aaatcagcta ccacacccag 2340
67 cacaaggcc gcctcaagca cagaggctcc agtctgcattt ctttcaggaa gggcttgcaa 2400
68 gagaaggaca aggtgtggct gttgcgggag cagaagcgc agaagaaact ccgcaagctg 2460
69 ctcagaagcc tgcagaacaa cgacacgtgc agcatgccag gcctcacgtg cttcacccac 2520
70 gacaaccacg actggcagac ggcgccttcc tggacactgg ggccttctg tgcctgcacc 2580
71 agcgcacaca ataacacgtt cttgtgcattt aggaccatca atgagactca caatttcctc 2640
72 ttctgtgaat ttgcaactgg cttccttagag tactttgtatc tcaacacaga cccctaccag 2700
73 ctgtatgaatg cagtgaacac actggacagg gatgtcctca accagctaca cgtacagctc 2760
74 atggagctga ggagctgcaa gggttacaag cagtgttacc cccggactcg aaacatggac 2820
75 ctgggactta aagatggagg aagatgtatgg caatacaggc agtttcagcg tcgaaagtgg 2880
76 ccagaaatga agagacccctt ttcacaaatca ctgggacaac tggggaaagg ctgggaaagg 2940
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78 tggaaaaacca tgggggtgat ttccagcaga cctgtctat tggccaggag gcctgagaaa 3060
79 gcaaggcacgc actctcagtc aacatgacag attctggagg ataaccagca ggagcagaga 3120
80 taacttcagg aagtccattt ttgccttc ttttgcattt gattataacctt caccagctgc 3180
81 acaaaaatgca ttttttcgtt tcaaaaaatgc accactaacc ctccccccaga agtccacaaa 3240
82 ggaaaaacggg gagagcgagc gagagagatt tccttgaaa tttctcccaa gggcgaaagt 3300
83 cattggaaatt tttaaatcat agggggaaaag cagtctgtt ctaaatccctt ttattttttt 3360
84 gtttgcac aaagaaggaa ctaagaagca ggacagaggc aacgtggaga ggctgaaaac 3420
85 agtgcagaga cgtttgacaa tgagtctgtt gcacaaaaga gatgacattt acctagcact 3480
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89 <210> SEQ ID NO: 2

90 <211> LENGTH: 870

91 <212> TYPE: PRT

92 <213> ORGANISM: Homo sapiens

94 <400> SEQUENCE: 2

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96	1					5				10					15	
98	Ser	Leu	Leu	Gly	Gly	Ser	Ser	Ala	Phe	Leu	Ser	His	His	Arg	Leu	Lys
99										25				30		
101	Gly	Arg	Phe	Gln	Arg	Asp	Arg	Arg	Asn	Ile	Arg	Pro	Asn	Ile	Ile	Leu
102										40				45		
104	Val	Leu	Thr	Asp	Asp	Gln	Asp	Val	Glu	Leu	Gly	Ser	Met	Gln	Val	Met
105										55				60		
107	Asn	Lys	Thr	Arg	Arg	Ile	Met	Glu	Gln	Gly	Gly	Thr	His	Phe	Ile	Asn
108	65						70			75					80	
110	Ala	Phe	Val	Thr	Thr	Pro	Met	Cys	Cys	Pro	Ser	Arg	Ser	Ser	Ile	Leu
111										85				90		95
113	Thr	Gly	Lys	Tyr	Val	His	Asn	His	Asn	Thr	Tyr	Thr	Asn	Asn	Glu	Asn
114										100				105		110
116	Cys	Ser	Ser	Pro	Ser	Trp	Gln	Ala	Gln	Glu	Ser	Arg	Thr	Phe	Ala	

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117	115	120	125													
119	Val	Tyr	Leu	Asn	Ser	Thr	Gly	Tyr	Arg	Thr	Ala	Phe	Phe	Gly	Lys	Tyr
120	130	135	140													
122	Leu	Asn	Glu	Tyr	Asn	Gly	Ser	Tyr	Val	Pro	Pro	Gly	Trp	Lys	Glu	Trp
123	145	150	155	160												
125	Val	Gly	Leu	Leu	Lys	Asn	Ser	Arg	Phe	Tyr	Asn	Tyr	Thr	Leu	Cys	Arg
126	165	170	175													
128	Asn	Gly	Val	Lys	Glu	Lys	His	Gly	Ser	Asp	Tyr	Ser	Lys	Asp	Tyr	Leu
129	180	185	190													
131	Thr	Asp	Leu	Ile	Thr	Asn	Asp	Ser	Val	Ser	Phe	Phe	Arg	Thr	Ser	Lys
132	195	200	205													
134	Lys	Met	Tyr	Pro	His	Arg	Pro	Val	Leu	Met	Val	Ile	Ser	His	Ala	Ala
135	210	215	220													
137	Pro	His	Gly	Pro	Glu	Asp	Ser	Ala	Pro	Gln	Tyr	Ser	Arg	Leu	Phe	Pro
138	225	230	235	240												
140	Asn	Ala	Ser	Gln	His	Ile	Thr	Pro	Ser	Tyr	Asn	Tyr	Ala	Pro	Asn	Pro
141	245	250	255													
143	Asp	Lys	His	Trp	Ile	Met	Arg	Tyr	Thr	Gly	Pro	Met	Lys	Pro	Ile	His
144	260	265	270													
146	Met	Glu	Phe	Thr	Asn	Met	Leu	Gln	Arg	Lys	Arg	Leu	Gln	Thr	Leu	Met
147	275	280	285													
149	Ser	Val	Asp	Asp	Ser	Met	Glu	Thr	Ile	Tyr	Asn	Met	Leu	Val	Glu	Thr
150	290	295	300													
152	Gly	Glu	Leu	Asp	Asn	Thr	Tyr	Ile	Val	Tyr	Thr	Ala	Asp	His	Gly	Tyr
153	305	310	315	320												
155	His	Ile	Gly	Gln	Phe	Gly	Leu	Val	Lys	Gly	Lys	Ser	Met	Pro	Tyr	Glu
156	325	330	335													
158	Phe	Asp	Ile	Arg	Val	Pro	Phe	Tyr	Val	Arg	Gly	Pro	Asn	Val	Glu	Ala
159	340	345	350													
161	Gly	Cys	Leu	Asn	Pro	His	Ile	Val	Leu	Asn	Ile	Asp	Leu	Ala	Pro	Thr
162	355	360	365													
164	Ile	Leu	Asp	Ile	Ala	Gly	Leu	Asp	Ile	Pro	Ala	Asp	Met	Asp	Gly	Lys
165	370	375	380													
167	Ser	Ile	Leu	Lys	Leu	Leu	Asp	Thr	Glu	Arg	Pro	Val	Asn	Arg	Phe	His
168	385	390	395	400												
170	Leu	Lys	Lys	Met	Arg	Val	Trp	Arg	Asp	Ser	Phe	Leu	Val	Glu	Arg	
171	405	410	415													
173	Gly	Lys	Leu	Leu	His	Lys	Arg	Asp	Asn	Asp	Lys	Val	Asp	Ala	Gln	Glu
174	420	425	430													
176	Glu	Asn	Phe	Leu	Pro	Lys	Tyr	Gln	Arg	Val	Lys	Asp	Leu	Cys	Gln	Arg
177	435	440	445													
179	Ala	Glu	Tyr	Gln	Thr	Ala	Cys	Glu	Gln	Leu	Gly	Gln	Lys	Trp	Gln	Cys
180	450	455	460													
182	Val	Glu	Asp	Ala	Thr	Gly	Lys	Leu	Lys	Leu	His	Lys	Cys	Lys	Gly	Pro
183	465	470	475	480												
185	Met	Arg	Leu	Gly	Gly	Ser	Arg	Ala	Leu	Ser	Asn	Leu	Val	Pro	Lys	Tyr
186	485	490	495													
188	Tyr	Gly	Gln	Gly	Ser	Glu	Ala	Cys	Thr	Cys	Asp	Ser	Gly	Asp	Tyr	Lys
189	500	505	510													

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191 Leu Ser Leu Ala Gly Arg Arg Lys Lys Leu Phe Lys Lys Tyr Lys
 192 515 520 525
 194 Ala Ser Tyr Val Arg Ser Arg Ser Ile Arg Ser Val Ala Ile Glu Val
 195 530 535 540
 197 Asp Gly Arg Val Tyr His Val Gly Leu Gly Asp Ala Ala Gln Pro Arg
 198 545 550 555 560
 200 Asn Leu Thr Lys Arg His Trp Pro Gly Ala Pro Glu Asp Gln Asp Asp
 201 565 570 575
 203 Lys Asp Gly Gly Asp Phe Ser Gly Thr Gly Gly Leu Pro Asp Tyr Ser
 204 580 585 590
 206 Ala Ala Asn Pro Ile Lys Val Thr His Arg Cys Tyr Ile Leu Glu Asn
 207 595 600 605
 209 Asp Thr Val Gln Cys Asp Leu Asp Leu Tyr Lys Ser Leu Gln Ala Trp
 210 610 615 620
 212 Lys Asp His Lys Leu His Ile Asp His Glu Ile Glu Thr Leu Gln Asn
 213 625 630 635 640
 215 Lys Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Lys Arg
 216 645 650 655
 218 Pro Glu Glu Cys Asp Cys His Lys Ile Ser Tyr His Thr Gln His Lys
 219 660 665 670
 221 Gly Arg Leu Lys His Arg Gly Ser Ser Leu His Pro Phe Arg Lys Gly
 222 675 680 685
 224 Leu Gln Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys
 225 690 695 700
 227 Lys Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys
 228 705 710 715 720
 230 Ser Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn Gln His Trp Gln
 231 725 730 735
 233 Thr Ala Pro Phe Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr Ser Ala
 234 740 745 750
 236 Asn Asn Asn Thr Tyr Trp Cys Met Arg Thr Ile Asn Glu Thr His Asn
 237 755 760 765
 239 Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Leu
 240 770 775 780
 242 Asn Thr Asp Pro Tyr Gln Leu Met Asn Ala Val Asn Thr Leu Asp Arg
 243 785 790 795 800
 245 Asp Val Leu Asn Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys
 246 805 810 815
 248 Lys Gly Tyr Lys Gln Cys Asn Pro Arg Thr Arg Asn Met Asp Leu Gly
 249 820 825 830
 251 Leu Lys Asp Gly Gly Ser Tyr Glu Gln Tyr Arg Gln Phe Gln Arg Arg
 252 835 840 845
 254 Lys Trp Pro Glu Met Lys Arg Pro Ser Ser Lys Ser Leu Gly Gln Leu
 255 850 855 860
 257 Trp Glu Gly Trp Glu Gly
 258 865 870
 261 <210> SEQ ID NO: 3
 262 <211> LENGTH: 2610
 263 <212> TYPE: DNA

10/24/01

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Input Set : A:\10147611.app
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310 CCGG, 313 <210> SEQ ID NO: 4
W--> 314 <400> SEQUENCE: 4
W--> 315 000

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/970,287

DATE: 10/24/2001
TIME: 16:28:58

Input Set : A:\10147611.app
Output Set: N:\CRF3\10242001\1970287.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:314 M:283 W: Missing Blank Line separator, <400> field identifier
L:315 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (4) SEQUENCE:
L:319 M:283 W: Missing Blank Line separator, <400> field identifier
L:320 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:
L:324 M:283 W: Missing Blank Line separator, <400> field identifier
L:325 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6) SEQUENCE:
L:329 M:283 W: Missing Blank Line separator, <400> field identifier
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L:335 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:339 M:283 W: Missing Blank Line separator, <400> field identifier
L:340 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:344 M:283 W: Missing Blank Line separator, <400> field identifier
L:345 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE: